App No.: 09/830762
Docket No.: DFN-031US
Inventor: Margaret Shipp et al.
Title: LYMPHOMA ASSOCIATED MOLECULES AND USES
THEREFOR   replacement pages

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BAL human cDNA

5'UTR:
GGGCTTCGTGTTCCTGGGTGCTGACCGTGCACTCCCCGCCGCCCGAGGACTTAGAGCTCTGGAAGT
AGCTCTCCAGCTTCCTTCGTACTCGGGGGCCGGACTTGTACACCCGCACGAGGAGCGGGGACGGC
GGGCGCAGAAGTGGGCCACCATATCTGGAAACTACAGTCTATGCTTTGAAGCGCAAAAGGGAATA
AACATTTAAAGACTCCCCCGGGGACCTGGAGG

Coding: alternatively spliced sequence in bold characters

ATGGACTTTTCCATGGTGGCCGGAGCAGCAGCTTACAATGAAAAATCAG**GTAGGATTACCTCGCT**
CTCACTCTTGTTTCAGAAAGTCTTTGCTCAGATCTTTCCTCAGTGGAGAAAGGGGAATACAG
AAGAATGTCTCCCCTACAAGTGCTCAGAGACTGGTGCTCTTGGAGAAAACTATAGTTGGCAAAT
TCCCATTAACCACAATGACTTCAAAATTTTAAAAAATAATGAGCGTCAGCTGTGTGAAGTCCTCCA
GAATAAGTTTGGCTGTATCTCTACCCTGGTCTCTCCAGTTCAGGAAGGCAACAGCAAATCTCTGCA
AGTGTTCAGAAAAATGCTGACTCCTAGGATAGAGTTATCAGTCTGGAAAGATGACCTCACCACAC
ATGCTGTTGATGCTGTGGTGAATGCAGCCAATGAAGATCTTCTGCATGGGGGAGGCCTGGCCCTGG
CCCTGGTAAAAGCTGGTGGATTTGAAATCCAAGAAGAGAGCAAACAGTTTGTTGCCAGATATGGT
AAAGTGTCAGCTGGTGAGATAGCTGTCACGGGAGCAGGGAGGCTTCCCTGCAAACAGATCATCCA
TGCTGTTGGGCCTCGGTGGATGGAATGGGATAAACAGGGATGTACTGGAAAGCTGCAGAGGGCCA
TTGTAAGTATTCTGAATTATGTCATCTATAAAAATACTCACATTAAGACAGTAGCAATTCCAGCCT
TGAGCTCTGGGATTTTTCAGTTCCCTCTGAATTTGTGTACAAGACTATTGTAGAGACTATCCGGGT
TAGTTTGCAAGGGAAGCCAATGATGAGTAATTTGAAAGAAATTCACCTGGTGAGCAATGAGGACC
CTACTGTTGCTGCCTTTAAAGCTGCTTCAGAATTCATCCTAGGGAAGAGTGAGCTGGGACAAGAAA
CCACCCCTTCTTTCAATGCAATGGTCGTGAACAACCTGACCCTCCAGATTGTCCAGGGCCACATTG
AATGGCAGACGGCAGATGTAATTGTTAATTCTGTAAACCCACATGATATTACAGTTGGACCTGTGG
CAAAGTCAATTCTACAACAAGCAGGAGTTGAAATGAAATCGGAATTTCTTGCCACAAAGGCTAAA
CAGTTTCAACGGTCCCAGTTGGTACTGGTCACAAAAGGATTTAACTTGTTCTGTAAATATATATAC
CATGTACTGTGGCATTCAGAATTTCCTAAACCTCAGATATTAAAACATGCAATGAAGGAGTGTTTG
GAAAAATGCATTGAGCAAAATATAACTTCCATTTCCTTTCCTGCCCTTGGGACTGGAAACATGGAA
ATAAAGAAGGAAACAGCAGCAGAGATTTTGTTTGATGAAGTTTTAACATTTGCCAAAGACCATGT
AAAACACCAGTTAACTGTAAAATTTGTGATCTTTCCAACAGATTTGGAGATATATAAGGCTTTCAG
TTCTGAAATGGCAAAGAGGTCCAAGATGCTGAGTTTGAACAATTACAGTGTCCCCCAGTCAACCA
GAGAGGAGAAAAGAGAAAATGGGCTTGAAGCTAGATCTCCTGCCATCAATCTGATGGGATTCAAC
GTGGAAGAGATGTAGTGAGGCCCACGCATGGATCCAAAGAATCCTGAGTCTCCAGAACCACCACA
TCATTGAGAATAATCATATTCTGTACCTTGGGAGAAAGGAACATGACATTTTGTCTCAGCTTCAGA
AAACTTCAAGTGTCTCCATCACAGAAATTATCAGCCCAGGAAGGACAGAGTTAGAGATTGAAGGA
GCCCGGGCTGACCTCATTGAGGTGGTTATGAACATTGAAGATATGCTTTGTAAAGTACAGGAGGA
AATGGCAAGGAAAAAGGAGCGAGGCCTTTGGCGCTCGTTAGGACAGTGGACTATTCAGCAACAAA
AAACCCAAGACGAAATGAAAGAAAATATCATATTTCTGAAATGTCCTGTGCCTCCAACTCAAGAG
CTTCTAGATCAAAAGAAACAGTTTGAAAAATGTGGTTTGCAGGTTCTAAAGGTGGAGAAGATAGA
CAATGAGGTCCTTATGGCTGCCTTTCAAAGAAAGAAGAAATGATGGAAGAAAAACTGCACAGGC
AACCTGTGAGCCATAGGCTGTTTCAGCAAGTCCCATACCAGTTCTGCAATGTGGTATGCAGAGTTG
GCTTTCAAAGAATGTACTCGACACCTTGCGATCCAAAATACGGAGCTGGCATATACTTCACCAAGA
ACCTCAAAAACCTGGCAGAGAAGGCCAAGAAAATCTCTGCTGCAGATAAGCTGATCTATGTGTTT
GAGGCTGAAGTACTCACAGGCTTCTTCTGCCAGGGACATCCGTTAAATATTGTTCCCCCACCACTG
AGTCCTGGAGCTATAGATGGTCATGACAGTGTGGTTGACAATGTCTCCAGCCCTGAAACCTTTGTT
ATTTTTAGTGGCATGCAGGCTATACCTCAGTATTTGTGGACATGCACCCAGGAATATGTACAGTCA
CAAGATTACTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGG
CAGCCCTGTTGATTAA

3' UTR
TCTCTACATCATTTTAACAGCTGGTATGGCCTTACCTTGGGTGAACTAACCAAATAATGACCATCG
ATGGCTCAAAGAGTGGCTTGAATATATCCCATGGGTTATCTGTATGGACTGACTGGGTTATTGAAA
GGACTAGCCACATACTAGCATCTTAGTGCCTTTATCTGTCTTTATGTCTTGGGGTTGGGGTAGGTAG
ATACCAAATGAAACACTTTCAGGACCTTCCTTCCTCTTGCAGTTGTTCTTTAATCTCCTTTACTAGA
GGAGATAAATATTTTGCATATAATGAAGAAATTTTTCTAGTATATAACGCAGGCCTTTTATTTTCTA
AAATGATGATAGTATAAAAATGTTAGGATAACAGAATGATTTTAGATTTTCCAGAGAATATTATAA
AGTGCTTTAGGTATGAAAATAAATCATCTTTGTCTGATTAAAAAAAAAAAA

BAL human protein: alternatively spliced (Bold characters)

MDFSMVAGAAAYNEKS**GRITSLSLLFQKVFAQIFPQWRKGNTEECLPYKCS**ETGALGENYSW
QIPINHNDFKILKNNERQLCEVLQNKFGCISTLVSPVQEGNSKSLQVFRKMLTPRIELSVWKDDLTT
HAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAV
GPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKP
MMSNLKEIHLVSNEDPTVAAFKAASEFILGKSELGQETTPSFNAMVVNNLTLQIVQGHIEWQTADVIVN
SVNPHDITVGPVAKSILQQAGVEMKSEFLATKAKQFQRSQLVLVTKGFNLFCKYIYHVLWHSEFPKPQI
LKHAMKECLEKCIEQNITSISFPALGTGNMEIKKETAAEILFDEVLTFAKD
HVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNYSVPQSTREEKRENGLEARSPAINLMGFNVE
EMYEAHAWIQRILSLQNHHIIENNHILYLGRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEVV
MNIEDMLCKVQEEMARKKERGLWRSLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKC
GLQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPVSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDP
KYGAGIYFTKNLKNLAEKAKKISAADKLIYVFEAEVLTGFFCQGHPLNIVPPPLSPGAIDGHDSVVDNVS
SPETFVIFSGMQAIPQYLWTCTQEYVQSQDYSSGPMRPFAQHPWRGFASGSPVD

Fig. 1A

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BAL mouse cDNA:

5'UTR

```
AGGAACGGAAGTTTGGCGGGAACCCGGATTCCCAGGTTCAGGCCTCTCAAGGGTGGAGCGGAATA
GAGGGAAACAGGCCACCATCTCCTCGATCTACAGACTACACTTGGAAACACAAACAAATATAAAT
ATCTGAAGACCCACGTGGGACCTGAAGAATGGCCTATTAC
```

Coding region (shorter form only)

```
ATGGATACATGGGCGGCAGCTCCCGCCGAAAGACCAGCCAACAATTCTCTTGAAGAACATTATAG
ATGGCAAATTCCCATTAAACACAATGTCTTCGAAATTTTAAAGAGCAATGAGAGTCAGCTATGTGA
AGTCCTCCAAAATAAGTTTGGATGCATCTCTACCCTGAGCTGTCCAACTCTAGCAGGGAGCAGCTC
TCCTGCTCAGAGAGTCTTCAGAAGGACCCTGATCCCTGGGATAGAGTTATCTGTCTGGAAGGATGA
CCTTACCAGACACGTTGTTGATGCTGTGGTGAACGCAGCCAATGAAAACCTTTTGCATGGAAGTGG
CCTGGCCGGAAGCTTGGTGAAAACTGGTGGCTTTGAAATCCAAGAAGAGAGCAAAAGAATCATTG
CCAACGTTGGTAAAATCTCAGTTGGTGGAATCGCTATCACCGGTGCGGGGAGACTTCCTTGCCATT
TGATTATCCATGCGGTTGGACCTCGGTGGACAGTTACGAACAGCCAGACAGCTATCGAATTACTGA
AATTTGCCATTAGGAACATTCTAGATTATGTCACCAAATATGATCTACGCATTAAGACAGTAGCAA
TTCCAGCCCTGAGCTCTGGAATTTTCCAGTTCCCTCTGGATTTGTGTACAAGCATAATTTTAGAAAC
TATCCGGCTTTATTTCCAAGACAAGCAAATGTTCGGTAATTTGAGAGAGATTCATCTGGTGAGCAA
TGAGGACCCCACTGTTGCGTCCTTTAAATCCGCCTCAGAAAGCATCCTAGGGAGGGACCTGAGCTC
TTGGGGGGGTCCAGAAACTGACCCTGCTTCCACCATGACTCTTCGCATCGGCCGGGCCTGACTCT
CCAGATTGTCCAAGGCTGTATTGAAATGCAAACAACAGATGTAATTGGTAATTCTGGATACATGCA
GGATTTTAAATCAGGACGAGTGGCACAGTCGATTCTTAGACAAGCAGGGGTTGAAATGGAAAAGG
AACTTGACAAGGTTAACCTGTCCACAGATTATCAAGAGGTGTGGGTCACAAAAGGATTTAAATTGT
CCTGTCAGTATGTCTTCCATGTGGCATGGCATTCCCAAATCAACAAATACCAGATATTGAAAGATG
CAATGAAGTCCTGTCTAGAAAAATGCCTTAAACCAGATATAAATTCCATTTCCTTTCCTGCTCTCG
GGACAGGATTGATGGATTTGAAGAAGAGTACAGCAGCTCAGATAATGTTTGAGGAAGTTTTTGCA
TTTGCTAAAGAGCACAAGGAAAAAACGCTAACTGTAAAGATTGTGATCTTTCCAGTAGATGTGGA
GACGTACAAGATTTTTTATGCTGAAATGACAAAAAGGTCCAACGAGCTGAATCTCAGCGGTAATA
GTGGTGCTTTAGCCCTGCAGTGGTCCAGTGGGGAGCAAAGAAGAGGCGGCCTTGAAGCTGGATCT
CCTGCCATCAATCTCATGGGTGTAAAAGTGGGAGAGATGTGTGAGGCCCAGGAATGGATTGAAAG
GTTGCTGGTCTCCCTGGACCACCACATCATTGAGAATAATCATATTCTCTATCTTGGGAAAAAAGA
GCACGACGTGCTGTCTGAGCTCCAGACCAGCACAAGAGTCTCCATTTCAGAGACTGTCAGTCCAA
GAACGGCCACTTTGGAGATTAAAGGTCCCCAGGCTGACCTCATTGACGCAGTTATGAGGATTGAAT
GTATGCTGTGTGACGTTCAGGAAGAAGTGGCAGGAAAAAGGGAGAAAAATCTTTGGAGCTTGTCA
GGACAGGGGACCAACCAGCAAGAAAAACTGGATAAAATGGAAGAATCGTACACATTTCAACGAT
ACCCAGCATCATTAACTCAGGAACTTCAGGACCGAAAGAAACAGTTTGAAAAGTGTGGCTTGTGG
GTTGTGCAGGTGGAGCAGATAGACAATAAGGTGCTGCTGGCTGCCTTCCAAGAGAAGAAGAAAAT
GATGGAAGAGAGGACGCCAAAGGGATCTGGGAGCCAAAGGTTGTTTCAGCAGGTCCCACATCAGT
TCTGCAATACGGTGTGCAGAGTCGGCTTCCACAGAATGTATTCGACATCCTATAACCCAGTTTATG
GAGCCGGCATATATTTCACCAAGAGCCTCAAAAATCTAGCAGACAAGGTCAAGAAAACCTCAAGC
ACAGACAAGCTAATCTATGTGTTTGAGGCAGAAGTACTCACAGGGTCCTTCTGTCAGGGTAATTCC
TCAAATATCATCCCTCCACCATTGAGTCCTGGGGCCTTAGATGTCAATGACAGCGTAGTTGACAAT
GTTTCCAGCCCTGAAACCATTGTTGTTTTTAATGGCATGCAGGCCATGCCCCTGTACTTGTGGACTT
GCACACAGGATAGGACATTCTCACAGCATCCGATGTGGTCACAGGACTACTCATCAGGACCAGGA
ATGGTCTCTTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAGCTCTGTTTAG
```

3'UTR:

```
TGTCTACATCAGTTTAACAAGCAGAAGGGGTTGAGAGAACTGACAAAATGATAAATAACAGGTTA
CCTGTTCAGAATGATGGGGTCACTAAAGGCACCGACCACACACTAGCATCATAGTGCCTTTGTCTT
TACCTCTGGGCTTGACTGGGCAGATGCCAGCTAAAACTTCCTCACTGTCTT
```

Fig. 2

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TTCTATTTGAtATCTTTCATCTCCTTTCCTATAGGTGACAGCAAGAATACTTTATATAGAACAAGGA
TATTTTTTTCAAGCCTGTTATTTTCTAAAATGATAGCACAAACTAGGACAACAGGATGATTTCAGG
TTTTCTATATAATTTATAAAGTGCTTTGGATATCCAAATAAATCACCTTTGTCTGAGT

BAL mouse protein (shorter form):

MDTWAAAPAERPANNSLEEHYRWQIPIKHNVFEILKSNESQLCEVLQNKFGCISTLSCPTLAGSSS
PAQRVFRRTLIPGIELSVWKDDLTRHVVDAVVNAANENLLHGSGLAGSLVKTGGFEIQEESKRIIA
NVGKISVGGIAITGAGRLPCHLIIHAVGPRWTVTNSQTAIELLKFAIRNILDYVTKYDLRIKTVAIPA
LSSGIFQFPLDLCTSIILETIRLYFQDKQMFGNLREIHLVSNEDPTVASFKSASESILGRDLSSWGGP
ETDPASTMTLRIGRGLTLQIVQGCIEMQTTDVIGNSGYMQDFKSGRVAQSILRQAGVEMEKELDK
VNLSTDYQEVWVTKGFKLSCQYVFHVAWHSQINKYQILKDAMKSCLEKCLKPDINSISFPALGT
GLMDLKKSTAAQIMFEEVFAFAKEHKEKTLTVKIVIFPVDVETYKIFYAEMTKRSNELNLSGNSG
ALALQWSSGEQRRGGLEAGSPAINLMGVKVGEMCEAQEWIERLLVSLDHHIIENNHILYLGKKE
HDVLSELQTSTRVSISETVSPRTATLEIKGPQADLIDAVMRIECMLCDVQEEVAGKREKNLWSLS
GQGTNQQEKLDKMEESYTFQRYPASLTQELQDRKKQFEKCGLWVVQVEQIDNKVLLAAFQE K
KKMMEERTPKGSGSQRLFQQVPHQFCNTVCRVGFHRMYSTSYNPVYGAGIYFTKSLKNLADKV
KKTSSTDKLIYVFEAEVLTGSFCQGNSSNIIPPPLSPGALDVNDSVVDNVSSPETIVVFNGMQAMP
LYLWTCTQDRTFSQHPMWSQDYSSGPGMVSSLQSWEWVLNGSSV

Fig. 2A

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>_ BAL Human protein   819 aa vs.
>_ BAL Mouse protein   826 aa
scoring matrix: , gap penalties: -12/-2
61.5% identity;   Global alignment score: 3158

```
              10        20        30        40        50        60
610015 MDFSMVAGAAAYNEKSETGALGENYSWQIPINHNDFKILKNNERQLCEVLQNKFGCISTL
       ::    .  :::    :.   ...:  :.: ::::::.::  :.:::.::  ::::::::::::::
     _     MD----TWAAAPAERPANNSLEEHYRWQIPIKHNVFEILKSNESQLCEVLQNKFGCISTL
              10        20        30        40        50


              70        80        90       100       110
610015 VSPVQEGNSKSLQ-VFRKMLTPRIELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALV
       :.   :.:.  :   :::.  : :  ::::::::::  :.::::::::::.::::.::: .::
     _     SCPTLAGSSSPAQRVFRRTLIPGIELSVWKDDLTRHVVDAVVNAANENLLHGSGLAGSLV
              60        70        80        90       100       110


        120       130       140       150       160       170
610015 KAGGFEIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAVGPRWMEWDKQGCTGKLQ
       :.:::::::::::...:  ::..:.: ::.:::::::. ::::::::  ..:      :..
     _     KTGGFEIQEESKRIIANVGKISVGGIAITGAGRLPCHLIIHAVGPRWTVTNSQTAIELLK
        120       130       140       150       160       170


        180       190       200       210       220       230
610015 RAIVSILNYVIYKNTHIKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKPMMSNLKE
       ::  .::.::  . .:::::::::::::::::::::::.:::. :  : :.:.:  :::::.:
     _     FAIRNILDYVTKYDLRIKTVAIPALSSGIFQFPLDLCTSIILETIRLYFQDKQMFGNLRE
        180       190       200       210       220       230


        240       250       260       270       280       290
610015 IHLVSNEDPTVAAFKAASEFILGK---SELGQETTP--SFNAMVVNNLTLQIVQGHIEWQ
       ::::::::::::::.:::.:::.:::  :::.   :    ...  .  .::::::::  ::  :
     _     IHLVSNEDPTVASFKSASESILGRDLSSWGGPETDPASTMTLRIGRGLTLQIVQGCIEMQ
        240       250       260       270       280       290


        300       310       320       330       340       350
610015 TADVIVNSVNPHDITVGPVAKSILQQAGVEMKSEFLATKAKQFQRSQLVLVTKGFNLFCK
       :.::::  ::    .:.  : ::.:::.::::::::.:.:.      :..   : : ::::::.: :.
     _     TTDVIGNSGYMQDFKSGRVAQSILRQAGVEMEKEL--DKVNLSTDYQEVWVTKGFKLSCQ
        300       310       320       330       340       350


        360       370       380       390       400       410
610015 YIYHVLWHSEFPKPQILKHAMKECLEKCIEQNITSISFPALGTGNMEIKKETAAEILFDE
       :..::  :::.. : :::: :::  :::::::  :.:.::::::::::  :..:.:::.:.:.:
     _     YVFHVAWHSQINKYQILKDAMKSCLEKCLKPDINSISFPALGTGLMDLKKSTAAQIMFEE
        360       370       380       390       400       410


        420       430       440       450       460       470
610015 VLTFAKDHVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNYS---VPQSTREEKR
       :...:::.  ..  :::::.::::::.: ::  : .:.:.:..  :.... :  . : .:  :.:
     _     VFAFAKEHKEKTLTVKIVIFPVDVETYKIFYAEMTKRSNELNLSGNSGALALQWSSGEQR
        420       430       440       450       460       470
```

Fig. 3

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```
              480       490       500       510       520       530
610015 ENGLEARSPAINLMGFNVEEMYEAHAWIQRILSLQNHHIIENNHILYLGRKEHDILSQLQ
       ..::::  ::::::::: .: :: ::.  ::.:.:   .::::::::::::.::.:::.::
       RGGLEAGSPAINLMGVKVGEMCEAQEWIERLLVSLDHHIIENNHILYLGKKEHDVLSELQ
              480       490       500       510       520       530


              540       550       560       570       580       590
610015 KTSSVSITEIISPGRTELEIEGARADLIEVVMNIEDMLCKVQEEMARKKERGLWRSLGQW
       ..  :::.: .::  .  :::.: .::::.:: :: ::: ::::.: :.:..:: ::
       TSTRVSISETVSPRTATLEIKGPQADLIDAVMRIECMLCDVQEEVAGKREKNLWSLSGQG
              540       550       560       570       580       590


              600       610       620       630       640       650
610015 TIQQQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKCGLQVLKVEKIDNEVLMAAFQRK
       : ::.:  :.:.:.  :  . :.  :::: :.::::::::::: :...::.::::.::.:
       TNQQEKL-DKMEESYTFQRYPASLTQELQDRKKQFEKCGLWVVQVEQIDNKVLLAAFQEK
              600       610       620       630       640       650


              660       670       680       690       700       710
610015 KKMMEEKLHRQPVSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDPKYGAGIYFTKNLKNLA
       ::::::.  .     :.:::::::.:::::.::::::.::::: .: ::::::::.::::::
       KKMMEERTPKGSGSQRLFQQVPHQFCNTVCRVGFHRMYSTSYNPVYGAGIYFTKSLKNLA
              660       670       680       690       700       710


              720       730       740       750       760       770
610015 EKAKKISAADKLIYVFEAEVLTGFFCQGHPLNIVPPPLSPGAIDGHDSVVDNVSSPETFV
       .:..::  :...:::::.: ::::.   :::.: ::.:::::::.: .:::::::::::.:
       DKVKKTSSTDKLIYVFEAEVLTGSFCQGNSSNIIPPPLSPGALDVNDSVVDNVSSPETIV
              720       730       740       750       760       770


              780       790       800       810
610015 IFSGMQAIPQYLWTCTQE--YVQ----SQDYSSGPMRPFAQHPWRGFASGSPVD
       .:.::::.: :::::::.  . :    :::::::::  . . :.   .:: :
       VFNGMQAMPLYLWTCTQDRTFSQHPMWSQDYSSGPGMVSSLQSWEWVLNGSSV-
              780       790       800       810       820
```

Fig. 3A

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Comparison of:
(A) 7486572155.52.67.361 >_ BAL Human   3244n
(B) 7486572155.52.67.362 >_ BAL Mouse   3024n
using matrix file: DNA, gap penalties: -16/-4

71.7% identity in 2916 nt overlap; score: 5444

```
       370       380       390       400       410       420
    CCCTACAAGTGCTCAGAGACTGGTGCTCTTGGAGAAAACTATAGTTGGCAAATTCCCATT
    ::: : :   :  ::: :   : ::::::: :::: : :::::  :::::::::::::::
    CCCGCCGAAAGACCAGCCAACAATTCTCTTGAAGAACATTATAGATGGCAAATTCCCATT
       200       210       220       230       240       250

       430       440       450       460       470       480
    AACCACAATGACTTCAAAATTTTAAAAAATAATGAGCGTCAGCTGTGTGAAGTCCTCCAG
    :: ::::::::  :::: :::::::::::: :   :::::: :::::::  ::::::::::::::::
    AAACACAATGTCTTCGAAATTTTAAAGAGCAATGAGAGTCAGCTATGTGAAGTCCTCCAA
       260       270       280       290       300       310

       490       500       510       520       530       540
    AATAAGTTTGGCTGTATCTCTACCCTGGTCTCTCCAGTTCAGGAAGGCAACAGCAAATCT
    ::::::::::: ::  ::::::::::::::   ::  :::::  ::  : ::: : :::::      ::
    AATAAGTTTGGATGCATCTCTACCCTGAGCTGTCCAACTCTAGCAGGGAGCAGCTCTCCT
       320       330       340       350       360       370

       550       560       570       580       590       600
    CTGCA---AGTGTTCAGAAAAATGCTGACTCCTAGGATAGAGTTATCAGTCTGGAAAGAT
        ::   ::: ::::::::  :   ::::  :::  ::::::::::::::::  ::::::::  :::
    GCTCAGAGAGTCTTCAGAAGGACCCTGATCCCTGGGATAGAGTTATCTGTCTGGAAGGAT
       380       390       400       410       420       430

       610       620       630       640       650       660
    GACCTCACCACACATGCTGTTGATGCTGTGGTGAATGCAGCCAATGAAGATCTTCTGCAT
    ::::: :::: ::: :  ::::::::::::::: :::::::::::: : ::: ::::::
    GACCTTACCAGACACGTTGTTGATGCTGTGGTGAACGCAGCCAATGAAAACCTTTTGCAT
       440       450       460       470       480       490

       670       680       690       700       710       720
    GGGGGAGGCCTGGCCCTGGCCCTGGTAAAAGCTGGTGGATTTGAAATCCAAGAAGAGAGC
    ::  : :::::::::: :     :  :::: ::: :::::::  ::::::::::::::::::::::::::::::
    GGAAGTGGCCTGGCCGGAACCTTGGTGAAAACTGGTGGCTTTGAAATCCAAGAAGAGAGC
       500       510       520       530       540       550

       730       740       750       760       770       780
    AAACAGTTTGTTGCCAGATATGGTAAAGTGTCAGCTGGTGAGATAGCTGTCACGGGAGCA
    :::    :   ::::::::    :::::::: : :::::::::::  ::  :::  ::::  ::  ::
    AAAAGAATCATTGCCAACGTTGGTAAAATCTCAGTTGGTGGAATCGCTATCACCGGTGCG
       560       570       580       590       600       610
```

Fig. 4

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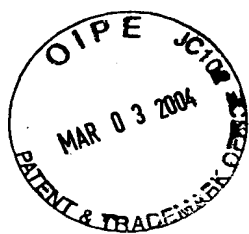
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```
         790         800         810         820         830         840
GGGAGGCTTCCCTGCAAACAGATCATCCATGCTGTTGGGCCTCGGTGGATGGAATGGGAT
::::: :::::  :::  :     :::  ::::::::: :::::  :::::::::::  :      :  :
GGGAGACTTCCTTGCCATTTGATTATCCATGCGGTTGGACCTCGGTGGACAGTTACGAAC
         620         630         640         650         660         670


         850         860         870         880         890         900
AAACAGGGATGTACTGGAAAGCTGCAGAGGGCCATTGTAAGTATTCTGAATTATGTCATC
:  :::  :  ::   : :   ::: :      ::::::     :  :::::   :::::::::  :
AGCCAGACAGCTATCGAATTACTGAAATTTGCCATTAGGAACATTCTAGATTATGTCACC
         680         690         700         710         720         730


         910         920         930         940         950         960
TATAAAAATACTCACATTAAGACAGTAGCAATTCCAGCCTTGAGCTCTGGGATTTTTCAG
:  :  ::    :  :::::::::::::::::::::::::::  :::::::::  :::::  :::
AAATATGATCTACGCATTAAGACAGTAGCAATTCCAGCCCTGAGCTCTGGAATTTTCCAG
         740         750         760         770         780         790


         970         980         990        1000        1010        1020
TTCCCTCTGAATTTGTGTACAAAGACTATTGTAGAGACTATCCGGGTTAGTTTGCAAGGG
::::::::::  ::::::::::::::  :   :::  ::::  :::::::::::  ::  :::  ::::
TTCCCTCTGGATTTGTGTACAAGCATAATTTTAGAAACTATCCGGCTTTATTTCCAAGAC
         800         810         820         830         840         850


        1030        1040        1050        1060        1070        1080
AAGCCAATGATGAGTAATTTGAAAGAAATTCACCTGGTGAGCAATGAGGACCCTACTGTT
::::  ::::  :    ::::::::::  :::   :::::::::::::::::::::::::   ::::::::
AAGCAAATGTTCGGTAATTTGAGAGAGATTCATCTGGTGAGCAATGAGGACCCCACTGTT
         860         870         880         890         900         910


        1090        1100        1110        1120        1130
GCTGCCTTTAAAGCTGCTTCAGAATTCATCCTAGGGAAGAG--TGAGCT-------GGGA
::  :::::::::  :  ::  ::::::   :::::::::::  :    :::::::        :::
GCGTCCTTTAAATCCGCCTCAGAAAGCATCCTAGGGAGGGACCTGAGCTCTTGGGGGGGT
         920         930         940         950         960         970


        1140        1150        1160        1170        1180
CAAGAAACCACCCCTTCTTTCA--ATG-CAATGGTCGTGAACAA---CCTGACCCTCCAG
:  :::::::    ::::  :::  ::   :::  :  :   :   : :      ::::::  ::::::
CCAGAAACTGACCCTGCTTCCACCATGACTCTTCGCATCGGCCGGGGCCTGACTCTCCAG
         980         990        1000         1010        1020        1030


   1190        1200        1210         1220        1230        1240
ATTGTCCAGGGCCACATTGAATGGCAGACGGCAGATGTAATTGTTAATTCTGTAAACCCA
::::::::  :::         ::::::   :::   ::  ::::::::::::  :::::::::  :  ::
ATTGTCCAAGGCTGTATTGAAATGCAAACAACAGATGTAATTGGTAATTCTGGATACATG
         1040        1050        1060        1070        1080        1090
```

Fig. 4A

App No.: 09/830762
Inventor: Margaret Shipp et al.
Title: LYMPHOMA ASSOCIATED MOLECULES AND USES
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```
      1250      1260      1270      1280      1290      1300
     CATGATATTACAGTTGGACCTGTGGCAAAGTCAATTCTACAACAAGCAGGAGTTGAAATG
     :: ::: ::: :   :::: ::::::: :::: :::::   :::::::::: :::::::::
     CAGGATTTTAAATCAGGACGAGTGGCACAGTCGATTCTTAGACAAGCAGGGGTTGAAATG
      1100      1110      1120      1130      1140      1150


      1310      1320      1330      1340      1350      1360
     AAATCGGAATTTCTTGCCACAAAGGCTAAACAGTTTCAACGGTCCCAGTTGGTACTGGTC
     :: :::: :::: :: ::: ::: : ::   :   : ::   ::: :::: 
     GAAAAGGAA---CTTGACA---AGGTTAACCTGTCCACAGATTATCAAGAGGTGTGGGTC
      1160             1170      1180      1190      1200


      1370      1380      1390      1400      1410      1420
     ACAAAAGGATTTAACTTGTTCTGTAAATATATATACCATGTACTGTGGCATTCAGAATTT
     ::::::::::::::: :::: :::: : ::: : : :::::::   :::::::: :: :
     ACAAAAGGATTTAAATTGTCCTGTCAGTATGTCTTCCATGTGGCATGGCATTCCCAAATC
      1210      1220      1230      1240      1250      1260


      1430      1440      1450      1460      1470      1480
     CCTAAACCTCAGATATTAAAACATGCAATGAAGGAGTGTTTGGAAAAATGCATTGAGCAA
     :::   ::::::::: ::: :::::::::::   ::: : :::::::::: :: : : :
     AACAAATACCAGATATTGAAAGATGCAATGAAGTCCTGTCTAGAAAAATGCCTTAAACCA
      1270      1280      1290      1300      1310      1320


      1490      1500      1510      1520      1530      1540
     AATATAACTTCCATTTCCTTTCCTGCCCTTGGGACTGGAAACATGGAAATAAAGAAGGAA
     ::::::: ::::::::::::::::: :: ::::: :::   ::::: : :::::::
     GATATAAATTCCATTTCCTTTCCTGCTCTCGGGACAGGATTGATGGATTTGAAGAAGAGT
      1330      1340      1350      1360      1370      1380


      1550      1560      1570      1580      1590      1600
     ACAGCAGCAGAGATTTTGTTTGATGAAGTTTTAACATTTGCCAAAGACCATGTAAAACAC
     ::::::::: :::: ::::::: ::::::::: ::::::: ::::: ::      :: :
     ACAGCAGCTCAGATAATGTTTGAGGAAGTTTTTGCATTTGCTAAAGAGCACAAGGAAAAA
      1390      1400      1410      1420      1430      1440


      1610      1620      1630      1640      1650      1660
     CAGTTAACTGTAAAATTTGTGATCTTTCCAACAGATTTGGAGATATATAAGGCTTTCAGT
     : ::::::::: :::: :::::::::::: :::: :::::: :: ::: ::: :
     ACGCTAACTGTAAAGATTGTGATCTTTCCAGTAGATGTGGAGACGTACAAGATTTTTTAT
      1450      1460      1470      1480      1490      1500


      1670      1680      1690      1700      1710
     TCTGAAATGGCAAAGAGGTCCAAGATGCTGAGTTTGAACAATTACAGTGT---------C
     ::::::::: :::: :::::::::: ::::: : : : :   : : :::: :
     GCTGAAATGACAAAAAGGTCCAACGAGCTGAATCTCAGCGGTAATAGTGGTGCTTTAGCC
      1510      1520      1530      1540      1550      1560
```

Fig. 4B

App No.: 09/830762   Docket No.: DFN-031US
Inventor: Margaret Shipp et al.
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```
     1720      1730      1740      1750      1760      1770
_    CCCCAGTCAACCAGAGAGGAGAAAAGAGAAAATGGGCTTGAAGCTAGATCTCCTGCCATC
     : :::: ::::: : :::: ::::: :   :: ::::::::: :::::::::::::::::
_    CTGCAGTGGTCCAGTGGGGAGCAAAGAAGAGGCGGCCTTGAAGCTGGATCTCCTGCCATC
     1570      1580      1590      1600      1610      1620


     1780      1790      1800      1810      1820      1830
_    AATCTGATGGGATTCAACGTGGAAGAGATGTAGTGAGGCCCACGCATGGATCCAAAGAAT
     ::::: ::::: : :: :::: ::::::::: ::::::::::: : ::::::: :::: :
_    AATCTCATGGGTGTAAAAGTGGGAGAGATGT-GTGAGGCCCAGGAATGGATTGAAAGGTT
     1630      1640      1650      1660      1670      1680


     1840      1850      1860      1870      1880      1890
_    CCTGAGTCTCCAGAACCACCACATCATTGAGAATAATCATATTCTGTACCTTGGGAGAAA
     ::: :: : ::::::::::::::::::::::::::::::::::::: :: ::::::: :::
_    GCTGGTCTCCCTGGACCACCACATCATTGAGAATAATCATATTCTCTATCTTGGGAAAAA
     1690      1700      1710      1720      1730      1740


     1900      1910      1920      1930      1940      1950
_    GGAACATGACATTTTGTCTCAGCTTCAGAAAACTTCAAGTGTCTCCATCACAGAAATTAT
     :: :: ::: : ::::: :::: :::: :   :::: ::::::::: :::: : : :
_    AGAGCACGACGTGCTGTCTGAGCTCCAGACCAGCACAAGAGTCTCCATTTCAGAGACTGT
     1750      1760      1770      1780      1790      1800


     1960      1970      1980      1990      2000      2010
_    CAGCCCAGGAAGGACAGAGTTAGAGATTGAAGGAGCCCGGGCTGACCTCATTGAGGTGGT
     ::: ::: ::: : :     :: ::::::: :::: ::: ::::::::::::::::: : ::
_    CAGTCCAAGAACGGCCACTTTGGAGATTAAAGGTCCCCAGGCTGACCTCATTGACGCAGT
     1810      1820      1830      1840      1850      1860


     2020      2030      2040      2050      2060      2070
_    TATGAACATTGAAGATATGCTTTGTAAAGTACAGGAGGAAATGGCAAGGAAAAAGGAGCG
     ::::: :::::: :::::: ::: : :: ::::: ::: ::::: : :::: ::::
_    TATGAGGATTGAATGTATGCTGTGTGACGTTCAGGAAGAAGTGGCAGGAAAAAGGGAGAA
     1870      1880      1890      1900      1910      1920


     2080      2090      2100      2110      2120      2130
_    AGGCCTTTGGCGCTCGTTAGGACAGTGGACTATTCAGCAACAAAAAACCCAAGACGAAAT
     :   :::::: ::: :: ::::::: :::: :   ::::: ::::: :   :: ::::
_    AAATCTTTGGAGCTTGTCAGGACAGGGGACCAACCAGCAAGAAAAA---CTGGATAAAAT
     1930      1940      1950      1960      1970      1980


     2140      2150      2160      2170      2180      2190
_    GAAAGAAAATATCATATTTCTGAAATGTCCTGTGCCTCCAACTCAAGAGCTTCTAGATCA
     : ::::: :: ::::: :: :: : : ::::::: :: :::: :: :
_    GGAAGAATCGTACACATTTCAACGATACCCAGCATCATTAACTCAGGAACTTCAGGACCG
     1990      2000      2010      2020      2030      2040
```

Fig. 4C

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Title: LYMPHOMA ASSOCIATED MOLECULES AND USES
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```
     2200      2210      2220      2230      2240      2250
     AAAGAAACAGTTTGAAAAATGTGGTTTGCAGGTTCTAAAGGTGGAGAAGATAGACAATGA
     ::::::::::::::::::: ::::: ::: :::: : ::::::::: ::::::::::::: :
     AAAGAAACAGTTTGAAAAGTGTGGCTTGTGGGTTGTGCAGGTGGAGCAGATAGACAATAA
     2050      2060      2070      2080      2090      2100

     2260      2270      2280      2290      2300      2310
     GGTCCTTATGGCTGCCTTTCAAAGAAAGAAGAAAATGATGGAAGAAAAACTGCACAGGCA
     ::: :: ::::::::::: ::: ::::::::::::::::::: :    :: : :
     GGTGCTGCTGGCTGCCTTCCAAGAGAAGAAGAAAATGATGGAAGAGAGGACGCCAAAGGG
     2110      2120      2130      2140      2150      2160

     2320      2330      2340      2350      2360      2370
     ACCTGTGAGCCATAGGCTGTTTCAGCAAGTCCCATACCAGTTCTGCAATGTGGTATGCAG
     : ::: ::::::: ::: ::::::::::: ::::::: : ::::::::::::: ::: :::::
     ATCTGGGAGCCAAAGGTTGTTTCAGCAGGTCCCACATCAGTTCTGCAATACGGTGTGCAG
     2170      2180      2190      2200      2210      2220

     2380      2390      2400      2410      2420      2430
     AGTTGGCTTTCAAAGAATGTACTCGACACCTTGCGATCCAAAATACGGAGCTGGCATATA
     ::: ::::::: :: ::::::::: ::::::: : :    : :::   :: ::::::: :::::::::
     AGTCGGCTTCCACAGAATGTATTCGACATCCTATAACCCAGTTTATGGAGCCGGCATATA
     2230      2240      2250      2260      2270      2280

     2440      2450      2460      2470      2480      2490
     CTTCACCAAGAACCTCAAAAAACCTGGCAGAGAAGGCCAAGAAAATCTCTGCTGCAGATAA
     ::::::::: ::::::::: :: ::::: :::: ::::::::: :::       :::: ::
     TTTCACCAAGAGCCTCAAAAAATCTAGCAGACAAGGTCAAGAAAACCTCAAGCACAGACAA
     2290      2300      2310      2320      2330      2340

     2500      2510      2520      2530      2540      2550
     GCTGATCTATGTGTTTGAGGCTGAAGTACTCACAGGCTTCTTCTGCCAGGGACATCCGTT
     ::: ::::::::::::::: ::::::::::::::::: : :::::: :::::   :: : :::
     GCTAATCTATGTGTTTGAGGCAGAAGTACTCACAGGGTCCTTCTGTCAGGGTAATTCCTC
     2350      2360      2370      2380      2390      2400

     2560      2570      2580      2590      2600      2610
     AAATATTGTTCCCCCACCACTGAGTCCTGGAGCTATAGATGGTCATGACAGTGTGGTTGA
     ::::::: : :: ::::::: :::::::::: :: ::::::   ::::::: :: :::::
     AAATATCATCCCTCCACCATTGAGTCCTGGGGCCTTAGATGTCAATGACAGCGTAGTTGA
     2410      2420      2430      2440      2450      2460

     2620      2630      2640      2650      2660      2670
     CAATGTCTCCAGCCCTGAAACCTTTGTTATTTTTAGTGGCATGCAGGCTATACCTCAGTA
     ::::::: ::::::::::::::::: ::::: :::::: ::::::::::::::: :: :: : :::
     CAATGTTTCCAGCCCTGAAACCATTGTTGTTTTTAATGGCATGCAGGCCATGCCCCTGTA
     2470      2480      2490      2500      2510      2520
```

Fig. 4D

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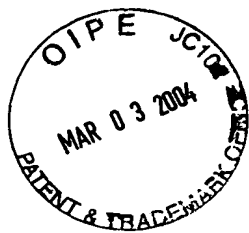
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```
        2680      2690      2700                                    2710      2720
    TTTGTGGACATGCACCCAGGA----ATATGTACA--------------GTCACAAGATTA
    ::::::::: ::::: :::::   : ::    ::              ::::: :: ::
    CTTGTGGACTTGCACACAGGATAGGACATTCTCACAGCATCCGATGTGGTCACAGGACTA
        2530      2540      2550      2560      2570      2580


        2730      2740      2750      2760      2770      2780
    CTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGGCAG
    :::::::::::::  :    :: : : ::: : :::   :  :: :: ::::::
    CTCATCAGGACCAGGAATGGTCTCTTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAG
        2590      2600      2610      2620      2630      2640


        2790      2800      2810      2820      2830      2840
    CCCTGTTGATTAATCTCTACATCATTTTAACAGCTGGTATGGCCTTACCTTGGGTGAACT
    : ::::    ::: : :::::::::: ::::::::  : : ::       ::: : :::::
    CTCTGT---TTAGTGTCTACATCAGTTTAACAAGCAGAAGGGG------TTGAGAGAACT
            2650      2660      2670      2680          2690


        2850      2860      2870      2880      2890      2900
    AACCAAATAATGACCATCGATGGCTCAAAGAGTGGCTTGAATATATCCCATGGGTTATCT
    :: :::: ::                    ::: :                :  ::::: ::
    GACAAAATGAT--------------AAATA------------------ACAGGTTACCT
        2700                                        2710


        2910      2920      2930      2940      2950      2960
    GTATGGACTGACTGGGTTATTGAAAGGACTAGCCACATACTAGCATCTTAGTGCCTTTAT
    ::   :: :::  :::: : : :: : ::     :::::: :::::::::: :::::::::
    GTTCAGAATGATGGGGTCACTAAAGGCACCGACCACACACTAGCATCATAGTGCCTTT--
    2720      2730      2740      2750      2760      2770


        2970      2980      2990      3000      3010      3020
    CTGTCTTTATGTCTTGGGGTTGGGGTAGGTAGATACCAAATGAAACACTTTCAGGACCTT
    ::::::::  :::   ::: : :    :.::  :::: :::   : ::::    :::    :: :
    --GTCTTTACCTCT--GGGCTTGACTGGGCAGATGCCAGCTAAAAC---TTCCTCACTGT
    2780      2790      2800   2810         2820      2830


        3030      3040      3050      3060      3070
    CCTTCCTCTTGCAGTTGTTCTTTAATCTCCTTTACTAGAGGAGATA-----AATATTTTG
    : :: :: :: :   ::::: ::::::::: ::: ::: :: :     :::: :::
    CTTTTCTATTTGACA---TCTTTCATCTCCTTTCCTATAGGTGACAGCAAGAATACTTTA
        2840      2850      2860      2870      2880
```

Fig. 4E

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```
    3080      3090      3100      3110      3120      3130
CATATAATGAAGAAATTTTTCTAGTATATAACGCAGGCCTTTTATTTTCTAAAATGATGA
 ::: ::   : ::  ::::::: :           ::  ::::  :::::::::::::::::
TATAGAACAAGGATATTTTTTT-----------CAAGCCTGTTATTTTCTAAAATGA---
  2890      2900                2910      2920      2930


    3140      3150      3160      3170      3180      3190
TAGTATAAAAATGTTAGGATAACAGAATGATTTTAGATTTTCCAGAGAATATTATAAAGT
 :::  : :::     ::::: ::::: :::::::: ::  ::::: : : ::: ::::::::
TAGCACAAAC----TAGGACAACAGGATGATTTCAGGTTTTCTATATAAT-TTATAAAGT
     2940         2950      2960      2970      2980


    3200      3210      3220      3230
GCTTTAGGTATGAAAATAAATCATCTTTGTCTGATT
 :::::  : :::    :::::::::::  :::::::::  :
GCTTTGGATATCCAAATAAATCACCTTTGTCTGAGT
2990      3000      3010      3020
```

Fig. 4F